Amendments to the Specification

Please replace paragraph [0023] with the following paragraph:

[0023] **Figure 1** is a representation of the structure and modular organization of WARP. **(A)** Nucleotide (SEQ ID NO: 41) and deduced amino acid sequence (SEQ ID NO: 21) of WARP. The stop codon at nucleotides 1275-1277 is marked with an asterix and a potential polyadenylation site at nucleotides 2279-2285 is shown in bold type. The position of potential N-linked (Asn^{264} and Asn^{359}) and O-linked (Ser^{148}, Thr^{361} and Thr^{400}) glycosylation sites are underlined. C-terminal cysteine residues (Cys^{369} and Cys^{393}) available for disulfide bond formation are circled. **(B)** The modular structure of WARP is shown using standard symbols to represent conserved ECM protein modules (Bork, P. and Bairoch, A., TIBS 20 poster C02, 1995). VA, VA-domain; F3, fibronectin type III domain; P/R. proline/arginine-rich segment. Approximate positions of N- and O-linked glycosylation sites and Cys residues, conserved in both mouse and human sequences, are indicated. **(C)** Alignment of the amino acid sequences of the human (SEQ ID NO:20) and mouse (SEQ ID NO:21) WARP protein sequences. The predicted N-terminal signal sequence is boxed and the position of potential N-linked (Asn^{264} and Asn^{359}) and O-linked (Ser^{148} and Thr^{361}) glycosylation sites conserved in both sequences are underlined. The conserved C-terminal cysteine residue (Cys^{393}) available for disulfide bond formation is boxed. Alignments were performed using CLUSTALW ~~(http://www.ch.embnet.org/~software/ClustalW.html)~~ (Thompson *et al.*, Nucl. Acids Res. 22 4673-4680, 1994). Sites where amino acids are identical in both sequences are marked with an asterisk, conserved substitutions are marked with a colon and semi-conserved substitutions with a full-stop.

Please replace paragraph [0024] with the following paragraph:

[0024] **Figure 2** is a representation of the alignment of VA domain and F3 repeats of WARP with homologous domains in other ECM proteins. Alignments were performed using CLUSTALW ~~(http://www.ch.embnet.org/software/ClustalW.html)~~ (Thompson *et al.*, 1994, *supra*). **(A)** Alignment of VA domains from several ECM and non-ECM proteins. Sequences

are matrilin-2 (SEQ ID NO:26) (GenBank Accession # NP_058042, amino acids 55-239), matrilin-4 (SEQ ID NO:27) (NP_038620, 34-218), matrilin-3 (SEQ ID NO:28) (NP_034900, 76-260), matrilin-1 (SEQ ID NO:29) (NP_034899, 43-227), collagen XIV (SEQ ID NO:22) (S78476, 156-337), collagen XII (SEQ ID NO:24) (NP_004361, 2321-2503), collagen VII (SEQ ID NO:23), collagen VI (SEQ ID NO:25), WARP (SEQ ID NO:31) (32-212), cochlin (SEQ ID NO:32) (O42163, 160-142), VLA-1 α-integrin (SEQ ID NO:30) (P56199, 142-334) and vwf (SEQ ID NO:33) (von Willebrand factor). Sites where amino acids are identical in all sequences are marked with an asterisk, conserved substitutions are marked with a colon and semi-conserved substitutions with a full-stop. **(B)** Alignment of F3 repeats from a sample of ECM proteins. Sequences are WARP F3 domain 2 (SEQ ID NO:36) (308-394), collagen XIV (SEQ ID NO:38) (S78476, 627-711), β4 integrin chain (SEQ ID NO:37) (NP_000204, 1461-1548), collagen XII SEQ ID NO:34) (NP_004361, 726-810), fibronectin (SEQ ID NO:35) (P11276, 1635-1720), WARP F3 domain 1 (SEQ ID NO:40) (215-301) and tenascin R (SEQ ID NO:39) (1589549, 867-951). Alignments are shaded using BOXSHADE ~~(http://www.ch.embnet.org/software/BOX_form.html)~~. Identical positions are shown within dark boxes and conserved substitutions in grey boxes.

Please replace paragraph [0028] with the following paragraph:

[0028] A summary of sequence identifiers is provided below:

SUMMARY OF SEQUENCE IDENTIFIERS

SEQ ID NO:	DESCRIPTION
1	Nucleotide sequence of human VA domain
2	Amino acid sequence of human VA domain
3	Nucleotide sequence of mouse WARP
4	Amino acid sequence of mouse WARP
5	Nucleotide sequence of human WARP
6	Amino acid sequence of human WARP
7	Nucleotide sequence of mouse VA domain
8	Amino acid sequence of human VA domain
9	NR1 primer
10	NF4 primer

SEQ ID NO:	DESCRIPTION
11	mHPRT1 primer
12	mHPRT2 primer
13	WARP probe
14	WARP primer
15	WARP primer
16	HPRT probe
17	HPRT primer
18	HPRT primer
19	genomic sequence of human WARP
20	Alignment of the amino acid sequences of the human and WARP protein sequence
21	Alignment of the amino acid sequence of the murine WARP protein sequence
22	collagen XIV [Figure 2A]
23	collagen VII [Figure 2A]
24	collagen XII [Figure 2A]
25	collagen VI [Figure 2A]
26	matrilin-2 [Figure 2A]
27	matrilin-4 [Figure 2A]
28	matrilin-3 [Figure 2A]
29	matrilin-1 [Figure 2A]
30	VLA [Figure 2A]
31	WARP [Figure 2A]
32	cochlin [Figure 2A]
33	vwf [Figure 2A]
34	coll XII F3-3 [Figure 2B]
35	fibronect F3-12 [Figure 2B]
36	WARP F3-2 [Figure 2B]
37	β4 integrin F3-3 [Figure 2B]
38	coll XIV F3-5 [Figure 2B]
39	tenascin-R F3-7 [Figure 2B]

SEQ ID NO:	DESCRIPTION
40	WARP F3-1 [Figure 2B]
41	WARP [Figure 1A]

Please replace paragraph [0143] with the following paragraph:

[0143] The mouse WARP open reading frame encodes a 415 amino acid protein with a predicted molecular weight of 45 kDa although the human sequence is slightly larger with a 3 amino acid (PRP) insertion in the C-terminal domain (Figure 1C). Both homologs contain an 18 amino acid signal sequence with a cleavage site between Ala^{18} and Arg^{19} as indicated by signal sequence prediction program SignalP (v2.0) ~~(http://genome.cbs.dtu.dk/services/SignalP-2.0)~~ (Nielsen *et al.*, *Protein Engineering* 10: 1-6, 1997). The signal sequence is followed by a VA-domain of approximately 200 amino acids with a putative MIDAS motif (Lee *et al.*, 1995, *supra*) and three potential O-linked sites at Ser^{148}, Thr^{362} and Thr^{401}, as predicted by NetOGlyc software ~~(http://genome.cbs.dtu.dk/services/NetOGlyc)~~ (Hansen *et al.*, *BioChem.* J. 308: 801-813, 1995) although only the first two are conserved in the human sequence (Figure 1C). Adjacent to the VA-domain are two fibronectin type III (F3) repeats of approximately 80 amino acids in length, each containing a potential N-linked glycosylation site at Asn^{264} and Asn^{359} that fits the consensus sequence NxS/T. The C-terminus at the end of the second F3 repeat is 21 amino acids in length (24 in the human sequence) and is rich in proline and arginine residues, but did not show homology to any other protein by extensive database searching. The domain structure of the WARP proteins is shown in Figure 1B.

Please replace paragraph [0153] with the following paragraph:

[0153] A human homolog of murine *WARP* was identified by database homology searching. ~~The nucleotide sequence (SEQ ID NO:5) and corresponding amino acid sequence (SEQ ID NO:6) are shown in Figure 6.~~

Please replace the current Sequence Listing with the Substitute Sequence Listing submitted herewith in paper form (30 pages) and in computer readable form (two copies of disk).